academicJournals

Vol. 11(33), pp. 3169-3177, 18 August, 2016
DOI: 10.5897/AJAR2016.11160
Article Number: D31747C60047
ISSN 1991-637X

http://www.academicjournals.org/AJAR

African Journal of Agricultural Research

Full Length Research Paper

Phenotypic traits detect genetic variability in Okra (*Abelmoschus esculentus*. L. Moench)

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Received 28 April, 2016; Accepted 16 June, 2016

There is low production of okra in Ghana due to lack of improved varieties and biotic constraints. This study was conducted to characterize okra genotypes to predict genetic variation in the crop. Field trial was conducted to determine genetic variability in 21 okra genotypes. The experiment was based on the randomized complete block design (RCBD) involving planting distance of 0.6 × 0.6 m. Thirty-one quantitative and qualitative data were used to generate a dendrogram. Variations in leaf shape, leaf rib colour, petiole colour, petal colour, colour of the darkest ridges and stem colour were distinctive among the okra genotypes. The mean plant height, canopy diameter, leaf length and breadth, petiole length, internode length, number of branches, days to 50% flowering and fruit yield differed significantly ($p \leq 0.05$) among the 21 okra genotypes. These were discriminated into three clusters in a dendrogram with GH3731 as the most diverse. UCCC1, UCCC2, UCCC3, UCCC4 and UCCC5 appeared genetically similar with low fruit yield but early maturity. However, GH5332 had a significantly ($p \leq 0.05$) the highest fruit yield of 11.88 t ha^{-1} but late maturing. UCCC5 or similar genotypes with early maturity trait can be hybridized with GH5332 to improve the yield and earliness.

Key words: Breeding, germplasm, genotypes, genetic diversity and hybridization.

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) of the family Malvaceae, is an important and widely cultivated annual crop in both the tropical and sub-tropical regions of the world (Eshiet and Brisibe, 2015; Ali et al., 2014). It is a vegetable rich in organic and inorganic nutrients that sustain human health and as feed for animals (Chattopadhyay et al., 2011; Ofoefule, 2001; Rahman et al., 2012; Wamanda, 2007; Siesmonsma and Kouame, 2004; Saifullah and Rabbani, 2009). In Ghana, okra is often consumed in the diet by both children and adults in

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both rural and urban communities. However, the yield of this crop is low due to lack of improved varieties, biotic and abiotic stresses. Yield potential of 2000 to 3000 kg ha^{-1} has been reported for Okra (MoFA, 2007), depending on the cultivar, harvesting frequency and period for harvesting (Cudjoe et al*.,* 2005). However, actual yields of okra are usually low and also decreased over the years in Ghana, in spite of its economic importance and health benefits (Asare-Bediako et al., 2014).

The development of new varieties with better adaptation and yield potential are crucial for sustainable production of okra. Genetic variation in okra is a necessary requirement to improve the crop. Omonhinmin and Osawaru (2005) reported that high degree of wide morphological variation was found among accessions of okra, especially in West African type. There are numerous cultivars of okra with varied plant height, degree of branching and pigmentation of the various parts, period of maturity, and pod shape and size (AdeOluwa and Kehinde, 2011). In addition, Bisht et al. (1995) observed that pigmentation and pubescence of stem, leaf, pods and seeds were important components of variability in okra germplasm.

Various types of okra in Ghana are cultivated in the savannah and forest agro-ecological zones that require assessment of their genotypes. Ahiakpa et al. (2013) has done some morphological characterization of okra in Ghana but lacked collections from the central region and inclusion of exotic genotypes. The current work considered collections from the central region and other regions of Ghana as well as Togo to enhance assessment of fully harness variability in the germplasm for breeding and conservation. Indeed, genetic variation may serve as recipe for controlled hybridization to improve the crop. Assessment of variable phenotypic traits of okra would be useful in predicting genetic diversity towards molecular characterization to establish the genetic structure of okra in Ghana. This will facilitate routine breeding and germplasm conservation of the crop. The objective of the current work was to explore phenotypic characteristics to predict genetic variability among 21 okra genotypes in Ghana and to establish basis for molecular characterization.

MATERIALS AND METHODS

Experimental site

The experiment was conducted at the Teaching and Research Farm of the School of Agriculture, at University of Cape Coast during the 2015 major crop season (June to October). This site is located within the coastal savannah vegetation zone, with Acrisol soil type and is a highly endemic site for viral diseases and flea beetle infestation. The area has a bi-modal rainy season from May to June and August to October with an annual rainfall ranging between 750 and 1000 mm and temperatures ranging between 23.2 and 33.2°C with an annual mean of 27.6°C (Owusu-Sekyere et al., 2011).

Plant

Twenty-one genotypes of okra (both landraces and improved) were used for the study (Table 1). These comprised of fifteen accessions from Plant Genetic Resource Research Institute (PGRR1) at Bunso (wide collections from regions of Ghana and Togo), four farmer varieties, a land race and an improved variety (Asontem) from the Central Region of Ghana. The local names and sources of 21 okra genotypes are shown in Table 1.

Field experiment

The randomized complete block design (RCBD) with twenty-one genotypes of okra was sown in four replications. A total land area of 1344 m^2 (84 × 16 m) was ploughed and harrowed to render the soil loose. It was then divided into four blocks and each block was further divided into 21 plots, with each plot measuring 3 × 3 m. A distance of 1.0 m was left as walkway between the blocks and 1 m between the plots. Planting was done in June, 2015. The 21 okra genotypes were sown directly at three seeds per hole at a planting distance of 0.6 × 0.6 m and a planting depth of not more than 0.5 cm. The seedlings were later thinned out leaving two seedlings per hill. Weed control was done as necessary using herbicides and a hoe (manual weeding). NPK fertilizer (15:15:15) was applied at a rate of 250 kg ha^{-1}. Watering was done when necessary using sprinklers.

Data collection and analysis

The quantitative and qualitative data were collected based on the International Plant Genetic Resource Institute (IPGRI, 1991) okra descriptor list and adopted the procedure by Ahiakpa et al. (2013) and Nwangburuka et al. (2011) with some modifications (Table 2). The quantitative data including plant height, canopy diameter, leaf length, breadth, and stem base diameter at first flowering stage and petiole length, fruit length and fruit girth were obtained using meter rule or tape measure. The number of branches and fruits per plant were counted and fresh weight of matured fruits were determined by electronic balance (Radwag, WPT 12C1, Poland). The qualitative parameters were determined by visual estimation and rated (Table 1).

Data on plant growth and yield parameters were subjected to one-way analysis of variance (ANOVA) to determine significant differences among the 21 okra genotypes. The means were separated by the least significant difference method, using GenStat Discovery version 4 (VSN International). The GenStat or Minitab 15 statistical software was used for all computations. The Pearson's correlation coefficients were estimated for the growth and yield parameters. The Eigen-vectors and factor scores were used respectively to measure the relative discriminative power of the PC-axes and their associated characters. The data involving 31 parameters (Table 2) were analyzed with the PowerMarker version 3.5 and the dendrogram generated in Molecular Evolutionary Genetics Analysis version 4 (MEGA4) to determine genetic relatedness among the okra genotypes (Tamura et al. 2007).

RESULTS AND DISCUSSION

Qualitative and quantitative characteristic variations exist among the 21 okra genotypes. Variations in matured leaf colour, leaf shape, leaf rib colour, petiole colour, petal colour, colour of the darkest ridges and stem colour were

Table 1. Sources of okra genotypes used for the study.

Accession number	Accession name	Country of origin (Location)
UCCC2	Odumase	Ghana (Fosu Odumase)
UCCC3	Antado	Ghana (Antado-KEEA)
UCCC4	Asontem	Ghana (Assin Fosu)
GH2026	Manshior	Togo
GH2052	Fetri (Ewe)	Togo
GH2057	Fetri	Togo
GH2063	Fetri	Togo
GH3731	Krotetenye	Ghana (Abortia Junction)
GH3734	Fetri	Ghana (Kpogadzi)
GH3760	Nkruma	Ghana (Nsapor)
GH4374	Nkruma	Ghana (Duabone No.1)
GH5302	Pɛbrɛnkruma	Ghana (Ayiogbe)
GH5321	-	Ghana (Pinihi)
GH5332	Bropo Asontem	Ghana (Fententaa)
GH5786	Tuagya	Ghana (Koranten)
GH5793	Ogye abatan	Ghana (Asikasu)
UCCC5	Kakumdo	Ghana (Kakumdo)
GH6105	Asontem	Ghana (Mankessim)
GH6211	Nkrumah	Ghana (Ashiaman)
UCCC6	UCC Campus	Ghana (UCC-Cape Coast)
UCCC1	Avalavi	Ghana (Assin Akonfodi)

distinctive differentiation characters. In addition, differences in flowering span, fruit colour, fruit shape and number of ridges per fruit, pubescence, position of fruits on main stem and branching position at main stem were evident among the okra genotypes (Table 3).

The mean plant height, canopy diameter, leaf length and breadth, petiole length, internode length and number of branches as well as days to first flowering, 50% flowering and fruit yield differed significantly ($p < 0.05$) among the 21 okra genotypes. However, the stem diameter did not show significant ($p > 0.05$) variation among the okra genotypes. The highest average plant height of 68.95 cm was noted for UCCC3 and the least plant height of 28.72 cm was for GH4374 (Table 4). Plant height at flowering and fruiting are of particular interest for breeding programmes, because the presence of plants with tall and thin stems will increase the rate of lodging near harvesting and this could lead to loss of dry matter and subsequent decrease in fruit yield (Esthiet and Brisibe, 2015). In fact, Verma (1993), Ariyo et al. (1987) and Perdosa (1983) intimated that plant height is controlled by genetic factors and is closely associated with number of flowering node, average fruits per plant and number of internodes.

The leaves of okra serve as the main sites for photosynthesis, an increase or a decrease in their size could affect production of assimilates in the crop. Larger size leaves in any okra genotype may have higher ability to intercept solar radiation to assume higher photosynthetic capacity, which may enhance growth and crop yield. GH3734 had the widest canopy diameter of 100.86 cm compared to the least of UCCC5 (59.14 cm). The highest leaf length of 21.82 cm was produced by GH3734 and the lowest of 14.84 cm was associated with UCCC5. The mean leaf breadth of 29.55 cm was the highest observed for GH3760 compared to the least average leaf breadth of 19.89 cm for UCCC5 (Table 4). According to Ahiakpa (2013), an increased leaf area index and a resultant higher fraction of intercepted radiation and its utilization efficiency may increase crop yield. Significant ($p < 0.05$) correlations were observed between leaf length and canopy diameter ($r = 0.72$), breadth and canopy diameter ($r = 0.53$), leaf length and breadth ($r = 0.65$), petiole length and canopy diameter ($r = 0.49$) and stem diameter and canopy diameter ($r = 0.70$) in the okra germplasm could be determinants for plant vigour and yield indicators. GH2026 had the longest internodes of 21.53 cm per plant compared with the shortest for UCCC4 (14.69 cm per plant).

The mean petiole length of 20.64 cm was the highest for GH2052 compared with that of the lowest average petiole length of 14.29 cm for UCCC5. GH2026 had highest mean internodes (21.53 cm) and number of branches (5), respectively. However, GH2057, GH2063, GH4372 and GH5793 had the least number of 2 branches per plant. Variations in petiole length, leaf size,

Table 2. Rating of morphological characters of the okra genotypes used for the study.

Character	Rating/Estimation
Seed colour (SC)	1 = Dark, 2 = Black, 3 = Whitish to dark, 4 = purple to black
Seed Shape (SSh)	1 = Roundness, 2 = Kidney, 3 = Shperical
Seed size (SS)	1 = Small, 2 = medium, 3 = Large
Branching position at main stem (BPMS)	1 = UOA- Unique orthotrop axis, 2 = DBO- densely branched all over, 3 = DBB- densely branched base
Mature leaf colour (MLS)	1 = Green, 2 = Green + red veins
Leaf shape (LSH)	From type 1 to 11
Length of Branches (LBr)	0 = No branches, 1 = branches rarely > 10cm
Leaf rib colour (LRC)	1 = Green, 2 = Green + red veins
Petiole colour (Ptc)	1 = Green, 2 = greenish-red, 3 = purple
Petal colour (PC)	1 = 1= Golden yellow, 2 = yellow
Colour of the darkest ridges (CDR)	1 = light, 2 = dark, 3 = light to dark
Stem colour (StC)	1 = Green, 2 = Green + purple tinge, 3 = purple
Flowering span (FSp)	1 = Single flowering, 2 = grouped flowering
Fruit colour (FC)	1 = Green, 2 = green + red spots, 3 = dark green-black, 4= green-yellow, 5 =purple
Fruit pubescence (FP)	1 = Smooth, 2 = little rough, 3 = downy + hairs
Fruit shape (FSh)	From type 1 to 15
Number of ridges/fruit (NR)	1 = 0, 2 = 5-12, 3 = 15 ridges
Position of fruit on main stem (PFMS)	1= intermediate, 2 = slightly falling, 3 = horizontal, 4 = erect, 5 = drooping
Plant height (PH)	-
Canopy diameter (CD)	-
Leaf length (LL)	-
Leaf breadth (LB)	-
Stem diameter (SD)	-
Petiole length (PL)	-
Internode length (IN)	-
Number of branches (NBr)	-
Fruit length (FL)	-
Fruit girth (FG)	-
Number of fruits per plant (NF)	-
Weight of fruits (WF)	-
Days to first flower (DF)	-
Days to 50 % flowering (DFF)	-

canopy diameter, number of branches and stem diameter may have implications for crop yield and stability to control lodging.

According to Ariyo and Odulaja (1991), variability in okra germplasm is more prominent in days to flowering, plant height and various fruit characteristics and these traits could be important in differentiating varieties of *A. esculentus*. Similarly, in the current study, fruit length, girth and weight as well as the days to first flowering and days to 50% flowering differ significantly ($p < 0.05$) among the 21 genotypes of okra (Table 5). However, UCCC1, UCCC2, UCCC3, UCCC4, and UCCC5 were very similar in early flowering and days to 50% maturity as well as average fruit number, weight and size. Generally, all okra genotypes with high vegetative growth delayed flowering and maturity. UCCC5 was first to flower at 47 days and attained 50% flowering at 53 days, respectively after sowing seeds, which were significantly early compared to others. On the contrary UCCC6 was very late to first flower at 139 days and 50% flowering at 141 days, which were significantly ($p < 0.05$) different from all the other okra genotypes.

In this study, the significantly ($p < 0.05$) high yielding okra genotype, GH5332, produced 20 fruits per plant, with the highest fruit weight of 11.88 t ha^{-1}, which compared well with the size of the fruits (mean fruit length of 14.2 cm, girth 20 mm, and weight of fruit per plant of 21.6 g) among the okra genotypes. However, GH5332 is late maturing with 50% flowering at 101 days. Indeed, Esthiet and Brisibe (2015) reported that fruit length, pod

Table 3. Qualitative parameters of 21 Okra genotypes

Genotype	SC	SSh	SS	BPMS	MLC	LSh	LBr	LRC	PtC	PC	CDR	StC	NES	FSp	FC	FP	FSh	NR/F	PFMS
GH2026	1	1	2	3	2	3	1	1	3	2	1	3	1	1	1	2	4	2	3
UCCC2	1	1	2	1	1	2	0	1	1	2	1	1	1	1	1	3	3	2	1
UCCC4	1	3	1	1	1	9	0	1	1	2	1	1	2	1	1	2	8	2	1
GH3760	3	2	3	2	2	6	0	1	3	2	1	2	1	2	1	1	7	1	3
GH 2057	3	1	3	2	2	1	1	1	1	2	1	1	1	2	1	1	4	2	3
GH 6105	3	3	3	2	1	1	0	1	3	2	1	1	2	2	3	1	7	1	3
UCCC3	1	1	2	1	1	9	0	1	1	2	1	1	1	1	1	2	3	2	2
GH 5332	3	1	3	3	2	1	1	2	3	2	1	2	2	1	5	1	7	0	5
UCCC6	2	2	3	2	2	3	0	1	1	2	1	1	1	1	4	1	3	2	5
GH5302	2	2	3	2	2	3	0	1	3	2	1	1	2	2	5	1	4	2	3
GH5786	3	3	2	2	2	1	1	1	3	2	1	2	2	2	1	2	4	2	2
GH4374	1	1	3	3	2	3	1	1	3	2	1	2	2	2	1	1	12	2	4
GH3731	2	3	1	1	2	3	0	2	3	1	2	3	2	2	5	1	8	1	5
UCCC1	1	1	2	2	1	6	0	1	1	2	1	1	2	1	1	2	3	2	4
GH 3734	1	2	1	1	1	4	0	1	1	2	1	1	2	1	1	3	12	2	4
GH 5321	3	1	2	2	1	3	1	1	2	2	1	1	2	1	1	2	15	2	1
GH 5793	2	2	3	3	2	3	1	1	2	2	1	1	1	2	1	1	3	2	5
GH 2063	1	2	3	3	2	1	1	1	3	2	1	2	2	2	1	3	3	2	1
GH 6211	1	1	2	2	2	3	0	1	3	2	1	1	1	1	1	3	12	2	4
GH 2057	3	1	3	2	2	1	1	1	1	2	2	1	2	2	5	3	3	2	1
UCCC5	1	1	3	2	2	3	1	1	3	1	1	2	2	2	1	2	3	2	3

Seed colour (SC), Seed Shape (SSh), Seed size (SS), Branching position at main stem (BPMS), Mature leaf colour (MLC), Leaf shape (LSH), Length of Branches (LBr), Leaf rib colour (LRC), Petiole colour (Ptc), Petal colour (PC), Colour of the darkest ridges (CDR), Stem colour (StC), Number of epicalyx segments (NES) Flowering span (FSp), Fruit colour (FC), Fruit pubescence (FP), Fruit shape (FSh), Number of ridges per fruit (NR) and Position of fruit on main stem (PFMS).

number and pod weight are the most important determinants of production or yield in okra. It has been suggested that the number of days and plant height at flowering are controlled by the same genetic variables (Choudhary et al., 2006; Hussain et al., 2006).

It is critical to consider early maturity in the phase of erratic rainfall as essential trait to complement yield for hybridization to produce climate-smart okra genotypes. Therefore, UCCC5 with very early flowering and fruiting traits can be hybridized with the high yielding but late maturing genotypes of GH5332 to improve the crop. A successful cross between unrelated varieties may result into an array of elite genotypes from which advantageous agronomic line may be selected (Ali et al., 2014).

The variation in the quantitative characteristics which accounted for the total variance includes number of fruits per plant, mean plant height, canopy diameter, leaf length, breadth, stem diameter, petiole length, internode length, and number of branches. The proportion contributed by each quantitative variable to determine the total variation within each Principal Component (PC) axis is shown in Table 6. The variations in the quantitative characters contributed significantly

Table 4. Variation in growth characteristics of 21 okra genotypes.

Accessions	PH (cm)	CD (cm)	LL (cm)	LB (cm)	SD (cm)	PL (cm)	IN (cm)	NBr
GH2026	30.47	77.05	17.96	23.92	3.62	19.44	21.53	5
GH2052	17.96	84.57	17.53	27.29	3.3	20.64	18.83	3
GH2057	40.5	85.7	20.57	29.36	3.93	19.5	17.89	2
GH2063	31.61	90.36	19.97	26.39	3.51	20.15	15.89	2
GH3731	41.88	74.44	17.92	22.5	3.44	17.06	18.09	3
GH3734	60.98	100.86	21.82	26.68	4.11	22.16	19.42	4
GH3760	37.08	83.32	20.44	29.55	3.28	21.56	18.71	3
GH4374	28.72	79.08	17.64	23.02	4.21	18.2	17.56	2
GH5302	34.38	87.73	20.59	27.3	3.92	20.46	20.5	3
GH5321	47.32	77.03	18.13	25.47	4.43	19.53	20.32	3
GH5332	42.61	76.41	18.06	25.88	3.23	19.04	16.78	3
GH5786	34.51	86.09	20.52	27.68	3.75	21.57	19.47	3
GH5793	37.24	85.75	20.72	28.46	3.31	17.6	17.2	2
GH6105	42.52	93.49	20.39	24.54	3.9	20.46	18.36	3
GH6211	59.81	79.07	21.03	21.9	3.44	15.47	20.36	3
UCCC1	76.65	70.85	17.11	22.36	2.88	17.82	19.93	3
UCCC2	57.64	75.01	17.35	19.64	3.05	15.76	20.11	3
UCCC3	68.95	79.15	17.59	23.02	3.08	18.48	19.19	3
UCCC4	56.63	81.39	17.58	22.68	3.24	18.25	14.69	3
UCCC5	40.64	59.14	14.84	19.89	2.64	14.29	17.41	3
UCCC6	35.67	87.93	20.47	28.88	3.61	20.29	14.97	3
SE	14.3	20.51	4.97	7.03	2.01	7.15	6.31	2.02
Lsd	6.62	9.49	2.3	3.25	-	3.31	2.92	0.94

Plant height (PH), Canopy diameter (CD), Leaf length (LL), Leaf breadth (LB), Stem diameter (SD), Petiole length (PL), Internode length (IN and Number of branches (NBr).

(Eigen vector ≥ 0.2) to the variation within each of the four PC-axes as 38.00, 14.90, 12.40 and 11.70% for PC1, PC2, PC3 and PC4, respectively. The cumulative proportion of variation explained by the first four PC-axes, 77.00% (Table 6) compared well with observations made by Campos et al. (2005) and Ogunbayo et al. (2005) that the PC-axes contributed 76.62 and 64.5% variations, respectively. Similarly, Ahiakpa et al. (2013) reported that the first four PC-axis contributed 82.97% of the variations in okra. The remaining six axes in the current study accounted for only 23.00% of the total variation. Indeed, canopy diameter, leaf length, breadth, stem diameter and petiole length contributed to the variation in PC1. Plant height, length of internodes and number of branches accounted for the variations observed in PC2 and fruit per plant as well as plant height contributed to the variations in PC4. These variations may suggest the existence of genetic diversity in okra that can be harnessed to improve the crop. Similar observation was made by Yonas et al. (2014).

The 21 okra genotypes were distinguished into 3 main clusters (I, II and III) in the dendrogram at 43% genetic dissimilarity based on 31 quantitative and qualitative morphological characters (Figure 1). All the clusters were made up of varied sub-clusters with the exception of Cluster II, which had a single okra genotype (4.8%) involving GH3731, but the most diverse of all. However, cluster III made of 33.3% of the 21 okra genotypes appeared more closely related, including GH3734, GH6211, UCCC1, UCCC2, UCCC3, UCCC4 and UCCC5, which may suggest genetic similarity. The remaining 61.9% of the okra genotypes were distinguished in cluster I, which is the largest and made up of all the okra genotypes collected from the national gene bank, the Plant Genetic Resources Research Institute at Bunso with the exception of UCCC6. At 25% genetic dissimilarity, all the 21 okra genotypes were fully distinguished in the dendrogram. The dendrogram generated from genetic distance matrices gave an overall pattern of variations and relatedness among the okra genotypes, which agreed with the observation made by Nwangburuka et al. (2011).

Indeed, the dendrogram offered distinctive synopsis of the genetic relatedness in the okra germplasm, which is in agreement with the observation made by Aliyu and Fawole (2001) as well as Aremu et al. (2007). According to Ahiakpa et al. (2013), there is a direct relation between the eco-geographical origins of okra collections and their

Table 5. Variation in the average fruit yield and phenology among 21 okra genotypes.

Genotype	Fruit length (cm)	Fruit girth (cm)	Number of fruits	Fruit weight (g)	Yield (t ha^{-1})	Days to first flowering	Days to 50% flowering
UCCC2	8.7	2.04	5	18.9	2.49	53	74
UCCC3	8.1	2.24	4	23.6	2.57	54	68
UCCC4	8.8	2.06	4	19.3	2.23	51	70
GH2026	8.3	2.7	7	16	3.77	96	112
GH2052	8.1	2	3	14.8	1.55	105	130
GH2057	8.6	2.98	6	23.6	4.41	77	80
GH2063	8.6	2.03	2	16.1	0.86	94	125
GH3731	6.6	2.66	3	18.9	1.39	74	92
GH3734	5.8	2.59	6	17	2.85	84	85
GH3760	12.4	2.16	5	26.8	3.43	66	93
GH4374	6.6	3.03	4	15.3	1.68	104	120
GH5302	7.9	2.18	4	13.6	1.59	111	135
GH5321	7	3.11	8	21.1	4.96	52	77
GH5332	14.2	2	20	21.4	11.88	97	101
GH5786	7.3	2.67	3	16.3	1.43	102	120
GH5793	7.8	2.45	4	14.7	1.5	109	129
UCCC5	8	2.11	5	20.8	2.9	47	53
GH6105	12.2	2.11	15	22.6	9.34	61	92
GH6211	6.5	2.44	3	17.9	1.61	56	80
UCCC6	8.5	2.12	10	13.9	3.75	139	141
UCCC1	9	1.88	5	17.8	2.36	51	78
Mean	8.52	2.36	6.0	18.59	3.26	80.14	97.86
Lsd	1	0.2	3.5	3.1	2.09	10.7	7.6

Table 6. Principal component analysis of the 21 okra genotype showing the factor scores, Eigen values and percentage total variance accounted for by the first four principal component axes.

Character	PC1	PC2	PC3	PC4
Fruit/plant	0.162	-0.456	-0.031	0.523
Plant Height (cm)	-0.124	0.348	-0.039	0.804
Canopy Diameter (cm)	0.447	0.099	0.119	0.172
Leaf Length (cm)	0.466	0.113	0.071	0.095
Leaf Breadth (cm)	0.419	-0.252	-0.179	-0.073
Stem Diameter (cm)	0.427	0.117	0.253	-0.013
Petiole Length (cm)	0.427	0.217	-0.239	-0.169
Length of Internodes (cm)	-0.028	0.688	0.225	-0.076
Number of Branches	0. 012	0.225	-0.880	0.014
Eigen value	3.42	1.34	1.11	1.06
% Total variance	38.00	14.90	12.40	11.70
Cumulative % variance	38.00	52.90	65.30	77.00

clustering patterns in Ghana. Similarly, in the current work, the okra collections from the central region of Ghana clustered together and differentiated from those obtained from the PGRRI of Bunso. In addition, the germplasm collections from Togo especially GH2057, GH2052 and GH2063 being stored in PGRRI may be genetically similar for their close relatedness in cluster I. The distribution of okra genotypes might be influenced by farmer-consumer preferences, as well as okra trade and germplasm collection activities.

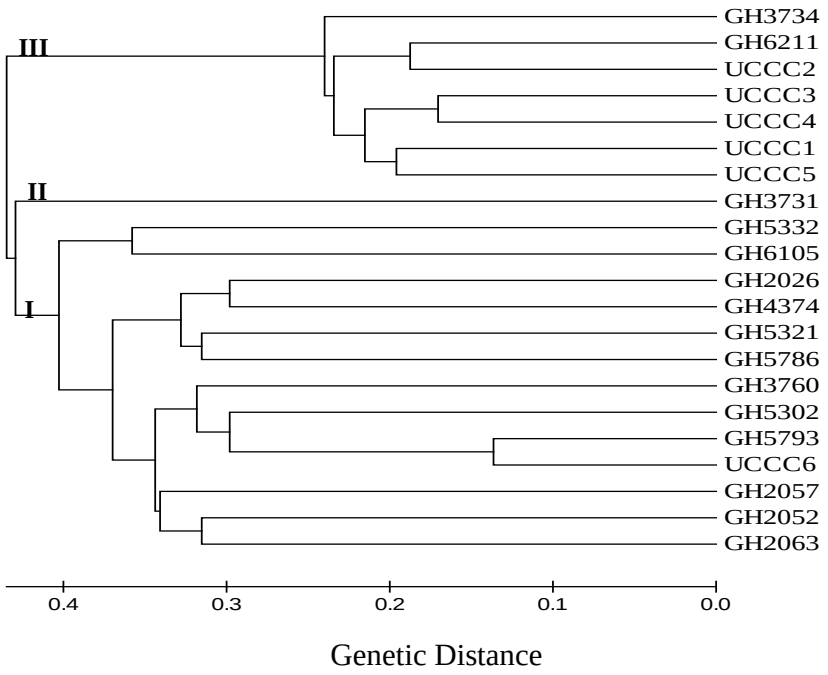

Figure 1. The UPGMA Dendrogram of genetic relationship among 21 okra genotypes based on 32 phenotypic characteristics.

Conclusions

The 31 quantitative and qualitative characters distinguished all the 21 okra genotypes without identifying clones. The discriminatory ability of the 31 characters was evident in clustering of the 21 okra genotypes in the dendrogram. UCCC1, UCCC2, UCCC3, UCCC4, UCCC5, GH6211 and GH3734 appeared more closely related. On the whole, the most diverse okra genotype was GH3731. UCCC5 had 50% flowering at 53 days which suggests very early maturity, followed by UCCC3 (68 days), UCCC2 (70 days). Though, GH5332 is late maturing with 50% flowering at 101 days, it produced a significantly ($p < 0.05$) highest fruit yield of 11.88 t/ha at a rate of 20 fruit per plant which compared well with the size of the fruits among the okra genotypes. UCCC5, UCCC3 and UCCC2 with early maturing but low yield can be hybridized with the high fruit producing, but late maturing okra genotypes of GH5332 and GH6105 to improve earliness in fruiting and adapt the crop to escape terminal drought. The most diverse genotype GH3731 could also be incorporated into breeding to broaden the genetic base of the crop. The almost 50% of the okra genotypes that produced fruits and also had large leaves suitable for use as leafy vegetables and to feed cattle could serve a dual purpose.

RECOMMENDATION

Though the phenotypic characters were useful to detect genetic variations in okra germplasm collections, they are not absolutely reliable since the traits can be influenced by the environment. Hence, there is a need to employ molecular markers to characterize the okra germplasm including exotic genotypes to establish the genetic structure of the crop and establish baseline information for breeding and conservation of the crop.

Conflict of Interests

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENT

The authors wish to acknowledge the University of Cape Coast in Ghana for sponsorship to conduct this initial genetic diversity study in okra.

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